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FEB 07 2002

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SEQUENCE LISTING

<110> Broun, Pierre

<120> METHOD FOR MODIFYING A BIOSYNTHETIC
PATHWAY

<130> 514442001200/MBI0032

<140> US 09/810,836

<141> 2001-03-16

<160> 14

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<213> Arabidopsis thaliana

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ctc tcc atc tct act act cca aag ccg aca acg acg acg gag aag aaa      98
Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys
          20              25              30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc      146
Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
          35              40              45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag      194
Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
          50              55              60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct      242
Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
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aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg      290
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp
          80              85              90              95

ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc      338
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gcc gtg agg aga ttc cgc ggc cgc gac gcc gtc act aac ttc aaa tct      386
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Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser	
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aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag	482
Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu	
145 150 155	
ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct	530
Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser	
160 165 170 175	
ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt	578
Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg	
180 185 190	
gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg	626
Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu	
195 200 205	
aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta	674
Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu	
210 215 220	
ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc	722
Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly	
225 230 235	
gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt	770
Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg	
240 245 250 255	
tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg	818
Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp	
260 265 270	
agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt	866
Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys	
275 280 285	
ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa	914
Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys	
290 295 300	
gtc cgg tct agt ccg gtt cag act gtg gtt agg cta ttc gga gtc aac	962
Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn	
305 310 315	
att ttc aat gtg agt aac gag aaa cca aac gac gtc gca gta gag tgt	1010
Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys	
320 325 330 335	
gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt	1058
Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys	

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Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu *			
355	360		

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Ser	Ser	Pro	Ala	Thr	Ser	Met	Arg	Leu	Tyr	Arg	Met	Gly	Ser	Gly	
	35					40				45					
Gly	Ser	Ser	Val	Val	Leu	Asp	Ser	Glu	Asn	Gly	Val	Glu	Thr	Glu	Ser
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Arg	Lys	Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Val	Pro	Gln	Pro	Asn
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Gly	Arg	Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys	His	Gln	Arg	Val	Trp	Leu
			85					90						95	
Gly	Thr	Phe	Asn	Glu	Glu	Glu	Glu	Ala	Ala	Ser	Ser	Tyr	Asp	Ile	Ala
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Val	Asp	Gly	Asn	Asp	Ala	Glu	Ser	Ala	Phe	Leu	Asp	Ala	His	Ser	Lys
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Ala	Glu	Ile	Val	Asp	Met	Leu	Arg	Lys	His	Thr	Tyr	Ala	Asp	Glu	Phe
145					150					155					160
Glu	Gln	Ser	Arg	Arg	Lys	Phe	Val	Asn	Gly	Asp	Gly	Lys	Arg	Ser	Gly
			165					170						175	
Leu	Glu	Thr	Ala	Thr	Tyr	Gly	Asn	Asp	Ala	Val	Leu	Arg	Ala	Arg	Glu
		180						185					190		
Val	Leu	Phe	Glu	Lys	Thr	Val	Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu	Asn
	195						200					205			
Arg	Leu	Val	Ile	Pro	Lys	Gln	His	Ala	Glu	Lys	His	Phe	Pro	Leu	Pro
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Ala	Met	Thr	Thr	Ala	Met	Gly	Met	Asn	Pro	Ser	Pro	Thr	Lys	Gly	Val
225					230					235					240
Leu	Ile	Asn	Leu	Glu	Asp	Arg	Thr	Gly	Lys	Val	Trp	Arg	Phe	Arg	Tyr
			245					250						255	
Ser	Tyr	Trp	Asn	Ser	Ser	Gln	Ser	Tyr	Val	Leu	Thr	Lys	Gly	Trp	Ser
		260					265						270		
Arg	Phe	Val	Lys	Glu	Lys	Asn	Leu	Arg	Ala	Gly	Asp	Val	Val	Cys	Phe
	275					280					285				
Glu	Arg	Ser	Thr	Gly	Pro	Asp	Arg	Gln	Leu	Tyr	Ile	His	Trp	Lys	Val
	290					295					300				
Arg	Ser	Ser	Pro	Val	Gln	Thr	Val	Val	Arg	Leu	Phe	Gly	Val	Asn	Ile
305					310					315					320
Phe	Asn	Val	Ser	Asn	Glu	Lys	Pro	Asn	Asp	Val	Ala	Val	Glu	Cys	Val

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 Met Asp
 1

 ttt gac gag gag cta aat ctt tgt att acg aaa ggt aaa aat gtt gat 164
 Phe Asp Glu Glu Leu Asn Leu Cys Ile Thr Lys Gly Lys Asn Val Asp
 5 10 15

 cat tct ttt gga gga gaa gct tct tcc acg tcc cca aga tct atg aag 212
 His Ser Phe Gly Gly Glu Ala Ser Ser Thr Ser Pro Arg Ser Met Lys
 20 25 30

 aaa atg aag agt cct agt cgt cct aaa ccc tat ttc caa tcc tct tct 260
 Lys Met Lys Ser Pro Ser Arg Pro Lys Pro Tyr Phe Gln Ser Ser Ser
 35 40 45 50

 tct cct tat tcg tta gag gct ttc cct ttt tct ctc gat cca aca ctt 308
 Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro Thr Leu
 55 60 65

 cag aat cag caa caa caa ctc gga tca tac gtt ccg gta ctt gag caa 356
 Gln Asn Gln Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu Glu Gln
 70 75 80

 cga caa gac ccg aca atg caa ggc cag aag caa atg atc tcc ttt agt 404
 Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser Phe Ser
 85 90 95

 cct caa caa caa caa cag cag cag cag tat atg gcc cag tac tgg agt 452
 Pro Gln Gln Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr Trp Ser
 100 105 110

 gac aca ttg aat ctg agt cca aga gga aga atg atg atg atg atg agc 500
 Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met Met Ser
 115 120 125 130

 caa gaa gct gtt caa cct tac atc gca acg aag ctg tac aga gga gtg 548
 Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg Gly Val
 135 140 145

aga caa cgt caa tgg gga aaa tgg gtc gca gag atc cgt aag cca cga	596
Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys Pro Arg	
150 155 160	
agc agg gca cgt ctt tgg ctt ggt acc ttt gat aca gct gaa gaa gct	644
Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala	
165 170 175	
gcc atg gcc tac gac cgc caa gcc ttc aaa tta cga ggc cac agc gca	692
Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His Ser Ala	
180 185 190	
aca ctg aat ttc ccg gag cat ttt gtg aat aag gaa agc gag ctg cat	740
Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu Leu His	
195 200 205 210	
gat tca aac tcg tcg gat cag aaa gaa cct gaa acg cca cag cca agc	788
Asp Ser Asn Ser Ser Asp Gln Lys Glu Pro Glu Thr Pro Gln Pro Ser	
215 220 225	
gag gtt aac ttg gag agc aag gaa cta ccg gtg att gat gtt ggg aga	836
Glu Val Asn Leu Glu Ser Lys Glu Leu Pro Val Ile Asp Val Gly Arg	
230 235 240	
gag gaa ggt atg gct gag gca tgg tac aat gcc att aca tcg gga tgg	884
Glu Glu Gly Met Ala Glu Ala Trp Tyr Asn Ala Ile Thr Ser Gly Trp	
245 250 255	
ggt cct gaa agt cct ctt tgg gat gat ttg gat agt tct cat cag ttt	932
Gly Pro Glu Ser Pro Leu Trp Asp Asp Leu Asp Ser Ser His Gln Phe	
260 265 270	
tca tca gaa agc tca tct tct tct cct ctc tct tgt cct atg agg cct	980
Ser Ser Glu Ser Ser Ser Ser Pro Leu Ser Cys Pro Met Arg Pro	
275 280 285 290	
ttc ttt tga aaaagtttat aaaccacat tgtgtgttag gttatagttt	1029
Phe Phe *	
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tatcagtcac tatatgtgtc taccttttct ctgtatttct atcattatca ttgtttttat	1149
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Met Lys Lys Met Lys Ser Pro Ser Arg Pro Lys Pro Tyr Phe Gln Ser

aag cat cca aat ttt cga ggt gtc aga atg aga caa tgg gga aaa tgg 256
Lys His Pro Asn Phe Arg Gly Val Arg Met Arg Gln Trp Gly Lys Trp
45 50 55
gtg tcc gaa atc aga gag cca aaa aag aaa tca aga atc tgg ctc ggt 304
Val Ser Glu Ile Arg Glu Pro Lys Lys Lys Ser Arg Ile Trp Leu Gly
60 65 70
act ttc tcc acg gcg gag atg gcg gcg cgt gct cac gac gtg gca gct 352
Thr Phe Ser Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala
75 80 85
tta gcc atc aaa ggc ggt tct gca cat ctc aac ttc ccg gag ctc gct 400
Leu Ala Ile Lys Gly Gly Ser Ala His Leu Asn Phe Pro Glu Leu Ala
90 95 100
tat cac ctc cct aga cca gct agt gcc gac cct aaa gac atc caa gct 448
Tyr His Leu Pro Arg Pro Ala Ser Ala Asp Pro Lys Asp Ile Gln Ala
105 110 115 120
gcc gcc gcc gca gct gca gcc gct gtg gcc att gac atg gat gta gag 496
Ala Ala Ala Ala Ala Ala Ala Val Ala Ile Asp Met Asp Val Glu
125 130 135
acg tct tcg ccg tcg cca tct ccc aca gtt acg gaa acg tca tct ccg 544
Thr Ser Ser Pro Ser Pro Ser Pro Thr Val Thr Glu Thr Ser Ser Pro
140 145 150
gct atg ata gca ctc tcc gac gac gcg ttc tcc gat ctt cct gat ctc 592
Ala Met Ile Ala Leu Ser Asp Asp Ala Phe Ser Asp Leu Pro Asp Leu
155 160 165
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Leu Leu Asn Val Asn His Asn Ile Asp Gly Phe Trp Asp Ser Phe Pro
170 175 180
tat gaa gaa ccc ttc ctc tct caa agt tac tag aaactcaaaa ctatgtcggt 693
Tyr Glu Glu Pro Phe Leu Ser Gln Ser Tyr *
185 190
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aattgtatga tttattaatg gttgatgatt ttctttgtgt ggaacaatgt gtatgatacg 813
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<212> PRT

<213> Arabidopsis thaliana

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35 40 45

gct gct gct aga ttc gct aac aca ttc caa gac att gtc aag gga gaa	394
Ala Ala Ala Arg Phe Ala Asn Thr Phe Gln Asp Ile Val Lys Gly Glu	
100 105 110	
gaa gaa tcg ggt tta gta ccc gga tcc gag atc cga cca gag tct cct	442
Glu Glu Ser Gly Leu Val Pro Gly Ser Glu Ile Arg Pro Glu Ser Pro	
115 120 125	
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Ser Thr Ser Ala Ser Val Ala Thr Ser Thr Val Asp Tyr Asp Phe Ser	
130 135 140	
ttt ttg gat ttg ctt ccg atg aat ttc ggg ttt gat tcc ttc tcc gac	538
Phe Leu Asp Leu Leu Pro Met Asn Phe Gly Phe Asp Ser Phe Ser Asp	
145 150 155 160	
gac ttc tct ggc ttc tcc ggt ggt gat cga ttt aca gag att tta ccc	586
Asp Phe Ser Gly Phe Ser Gly Gly Asp Arg Phe Thr Glu Ile Leu Pro	
165 170 175	
atc gaa gat tac gga gga gag agt tta tta gat gaa tct ttg att ctt	634
Ile Glu Asp Tyr Gly Gly Glu Ser Leu Leu Asp Glu Ser Leu Ile Leu	
180 185 190	
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Trp Asp Phe *	
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35 40 45	
Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Gln	
50 55 60	
Phe Cys Leu Arg Gly Gly Asp Ala Asn Phe Asn Phe Pro Asn Asn Pro	
65 70 75 80	
Pro Ser Ile Ser Val Glu Lys Ser Leu Thr Pro Pro Glu Ile Gln Glu	
85 90 95	
Ala Ala Ala Arg Phe Ala Asn Thr Phe Gln Asp Ile Val Lys Gly Glu	
100 105 110	
Glu Glu Ser Gly Leu Val Pro Gly Ser Glu Ile Arg Pro Glu Ser Pro	
115 120 125	
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